

- b) determining whether the activity of the polypeptide is reduced or increased by the chemical compound and, where appropriate, and
- c) determining the compound which specifically reduces or increases the activity of the polypeptide.

A1
cont

17. (Amended) A method for finding a compound which alters the expression of polypeptides with the biological activity of a very long chain fatty acid elongase, comprising the steps of:

- a) contacting a host cell containing a nucleic acid coding for a polypeptide with the biological activity of a very long chain fatty acid elongase with a chemical compound or a mixture of chemical compounds,
- b) determining the polypeptide concentration, and
- c) determining the compound which specifically influences the expression of the polypeptide.

SEQ ID NO: 2

20. (Amended) A modulator of VLCFAE which are found by a method according to Claim 16.

SEQ ID NO: 2

A2

21. (Amended) A herbicidally active substance found by a method according to Claim 16.

23. (Amended) An plant item selected from the group consisting of transgenic plants, parts of plants, protoplasts, plant tissues and plant propagation materials, comprising an introduced nucleic acid coding for a polypeptide having SEQ ID NO: 2, wherein the intracellular concentration of a polypeptide according to Claim 14 is increased or reduced compared with the corresponding wild-type cells.

A3

24. (Amended) An plant item selected from the group consisting of plants, parts of plants, protoplasts, plant tissues or plant propagation materials, comprising a polypeptide having SEQ ID NO: 2 whose biological

A3
cont

activity or expression pattern is altered by comparison with the corresponding endogenous polypeptides.

Please add the following claims:

--25. A modulator of VLCFAE which are found by a method according to Claim 17.

A4

26. A herbicidally active substance found by a method according to Claim 17.

27. A method according to Claim 15, wherein the polypeptide comprises a sequence selected from the group consisting of:

- a) the sequence shown in SEQ ID NO: 2,
- b) sequences encoded by a nucleic acid having SEQ ID NO: 1,
- c) partial sequences of the sequences defined under a) or b) which still have the biological activity of a VLCFAE,
- d) sequences which have an identity of at least 60% with the sequences defined under a) to c),
- e) sequences which include the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2,
- f) sequences which have an identity of at least 60% with the sequences defined under e),
- g) sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2,
- h) sequences which have an identity of at least 60% with the sequences defined under g).

28. A method according to Claim 15, wherein the polypeptide comprises a sequence selected from the group consisting of:

- a) the sequence shown in SEQ ID NO: 2,
- b) sequences encoded by a nucleic acid having SEQ ID NO: 1,
- c) sequences which include the C-terminally localized active site of

- d) sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2,

29. A method according to Claim 16, wherein the polypeptide comprises a sequence selected from the group consisting of:

- a) the sequence shown in SEQ ID NO: 2,
- b) sequences encoded by a nucleic acid having SEQ ID NO: 1,
- c) partial sequences of the sequences defined under a) or b) which still have the biological activity of a VLCFAE,
- d) sequences which have an identity of at least 60% with the sequences defined under a) to c),
- e) sequences which include the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2,
- f) sequences which have an identity of at least 60% with the sequences defined under e),
- g) sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2, and
- h) sequences which have an identity of at least 60% with the sequences defined under g).

30. A method according to Claim 16, wherein the polypeptide comprises a sequence selected from the group consisting of:

- a) the sequence shown in SEQ ID NO: 2,
- b) sequences encoded by a nucleic acid having SEQ ID NO: 1,
- c) sequences which include the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2, and
- d) sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2.

31. A method according to Claim 17, nucleic acid comprises a sequence selected from the group consisting of:

- a) the sequence shown in SEQ ID NO: 1,
- b) sequences which code for a polypeptide comprising the amino acid sequence shown in SEQ ID NO: 2,

	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

- c) partial sequences at least 14 base-pairs long of the sequences defined under a) or b),
- d) sequences which hybridize to the sequences defined under a) or b),
- e) sequences which have an identity of at least 60% with the sequences defined under a) or b),
- f) sequences which code for the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2
- g) sequences which have an identity of at least 60% with the sequences defined under f),
- h) sequences which code for the specific N terminus of the polypeptide shown in SEQ ID NO: 2,
- i) sequences which have an identity of at least 60% with the sequences defined under h),
- j) sequences which are complementary to the sequences defined under a) to i), and
- k) sequences which, because of the degeneracy of the genetic code, code for the same amino acid sequence as the sequences defined under a) to h).

32. A method according to Claim 17, nucleic acid comprises a sequence selected from the group consisting of:

- a) the sequence shown in SEQ ID NO: 1,
- b) sequences which code for a polypeptide comprising the amino acid sequence shown in SEQ ID NO: 2,
- c) sequences which hybridize to the sequences defined under a) or b),
- d) sequences which code for the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2
- e) sequences which code for the specific N terminus of the polypeptide shown in SEQ ID NO: 2,
- f) sequences which are complementary to the sequences defined under a) to e), and

- g) sequences which, because of the degeneracy of the genetic code, code for the same amino acid sequence as the sequences defined under a) to f).

33. A transgenic plant comprising a nucleic acid comprises a sequence selected from the group consisting of:

- a) the sequence shown in SEQ ID NO: 1,
- b) sequences which code for a polypeptide comprising the amino acid sequence shown in SEQ ID NO: 2,
- c) sequences which code for the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2
- d) sequences which code for the specific N terminus of the polypeptide shown in SEQ ID NO: 2,
- e) sequences which are complementary to the sequences defined under a) to d), and
- f) sequences which, because of the degeneracy of the genetic code, code for the same amino acid sequence as the sequences defined under a) to e).

34. A transgenic plant according to Claim 33, comprising a nucleic acid comprises a sequence selected from the group consisting of:

- a) the sequence shown in SEQ ID NO: 1, and
- b) sequences which code for a polypeptide comprising the amino acid sequence shown in SEQ ID NO: 2.

35. A method of determining with a target compound binds to a nucleic acid sequence coding a very long chain fatty acid elongase, comprising the step of contacting the target compound with a nucleic acid comprising a sequence selected from the group consisting of:

- a) the sequence shown in SEQ ID NO: 1,
- b) sequences which code for a polypeptide comprising the amino acid sequence shown in SEQ ID NO: 2,
- c) partial sequences at least 14 base-pairs long of the sequences defined under a) or b)

- A4
cont
- d) sequences which hybridize to the sequences defined under a) or b),
 - e) sequences which have an identity of at least 60% with the sequences defined under a) or b),
 - f) sequences which code for the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2
 - g) sequences which have an identity of at least 60% with the sequences defined under f),
 - h) sequences which code for the specific N terminus of the polypeptide shown in SEQ ID NO: 2,
 - i) sequences which have an identity of at least 60% with the sequences defined under h),
 - j) sequences which are complementary to the sequences defined under a) to i), and
 - k) sequences which, because of the degeneracy of the genetic code, code for the same amino acid sequence as the sequences defined under a) to h).

36. A method according to Claim 35, wherein the nucleic acid comprising a sequence selected from the group consisting of:

- a) the sequence shown in SEQ ID NO: 1,
- b) sequences which code for a polypeptide comprising the amino acid sequence shown in SEQ ID NO: 2,
- c) sequences which hybridize to the sequences defined under a) or b),
- d) sequences which code for the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2,
- e) sequences which code for the specific N terminus of the polypeptide shown in SEQ ID NO: 2,
- f) sequences which are complementary to the sequences defined under a) to e), and
- g) sequences which, because of the degeneracy of the genetic code, code for the same amino acid sequence as the sequences defined under a) to f).

37. A method of determining whether a target compound binds to a very long chain fatty acid elongase polypeptide, comprising the step of contacting the target compound with a polypeptide comprising a sequence selected from the group consisting of:

- a) the sequence shown in SEQ ID NO: 2,
- b) sequences encoded by a nucleic acid having SEQ ID NO: 1,
- c) partial sequences of the sequences defined under a) or b) which still have the biological activity of a VLCFAE,
- d) sequences which have an identity of at least 60% with the sequences defined under a) to c),
- e) sequences which include the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2,
- f) sequences which have an identity of at least 60% with the sequences defined under e),
- g) sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2,
- h) sequences which have an identity of at least 60% with the sequences defined under g).

38. A method according to Claim 37, wherein the polypeptide comprises a sequence selected from the group consisting of:

- a) the sequence shown in SEQ ID NO: 2,
- b) sequences encoded by a nucleic acid having SEQ ID NO: 1,
- c) sequences which include the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2,
- d) sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2.

39. A method according to Claim 37, comprising the steps of :

- a) providing a labelled substrate of the polypeptide, and
- b) comparing the conversion of the labelled substrate incubated with the polypeptide in the presence of the target compound to

